

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2003, 21:39:07 ; Search time 51 Seconds  
(without alignments)  
2371.362 Million cell updates/sec

Title: US-09-815-923-4  
Perfect score: 3141  
Sequence: 1 MPSPDAPPAPAPPPDLDPAT.....TQREPVTSIRPADSLCNL 587

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp\_invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2314	73.7	581	5	023969 drosophila
2	1681	53.5	631	6	096GMA5
3	1629.5	51.9	617	11	08R212
4	1618	51.5	576	5	09V7R0
5	1615.5	51.4	631	5	09NB97
6	1615.5	51.4	631	5	0961H9
7	1609.5	51.2	635	13	09DGN5
8	1606	51.1	630	13	042482
9	1605.5	51.1	628	4	096KH8
10	1605	51.1	617	6	09MYW8
11	1597.5	50.9	617	11	063380
12	1592	50.7	567	11	09WTR3
13	1589	50.7	597	11	09WTR4
14	1585.5	50.5	671	5	09NSC7
15	1579.5	50.3	671	5	0963F3
16	1573	50.1	629	13	0902V1

17	1551	49.4	515	13	091802	0918q2 coturnix co
18	1545	49.2	620	6	09GJ77	09gjt7 saimiri sci
19	1545	49.2	620	6	09GJ76	09gjt6 macaca fasc
20	1538	49.0	619	11	09J341	09j341 mus musculu
21	1538	49.0	620	6	09GJ75	09gjt5 saimiri sci
22	1533	48.8	619	11	09R0X6	09r0x6 mus musculu
23	1497	47.7	670	5	09SVZ4	09svz4 trichoplusi
24	1448.5	46.1	572	6	09MYW7	09myw7 macaca mla
25	1374.5	43.8	791	11	091202	0912q2 mus musculu
26	1372	43.7	598	13	073771	073771 raja sp. ga
27	1360.5	43.3	598	13	091494	091494 torpedo cal
28	1340	42.7	629	13	09DE16	09de16 oreochromis
29	1331.5	42.4	625	13	091BH6	091bh6 cyprinus ca
30	1302	41.5	597	5	025512	025512 manduca sex
31	1301.5	41.4	608	5	09NM10	09nm10 trichoplusi
32	1272.5	40.5	640	11	08VBW1	08vbw1 mus musculu
33	1269	40.4	622	13	091503	091503 torpedo mar
34	1256.5	40.0	611	13	091502	091502 torpedo mar
35	1247	39.7	621	11	091W12	091w12 mus musculu
36	1244	39.6	614	11	08VC59	08vc59 mus musculu
37	1227	39.1	638	11	09JMA9	09jma9 mus musculu
38	1227	39.1	613	11	091Y60	091y60 mus musculu
39	1226	39.0	513	5	09V4E7	09v4e7 drosophila
40	1224	39.0	1201	5	09W1J0	09w1j0 drosophila
41	1221	38.9	638	11	09D317	09d317 mus musculu
42	1221	38.9	727	5	09U5A5	09u5a5 manduca sex
43	1215	38.7	602	4	08TCC2	08tcc2 homo sapien
44	1211.5	38.6	943	5	002003	002003 drosophila
45	1211.5	38.6	943	5	09VR07	09vr07 drosophila

## ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	581 AA.
Q23969	Q23969		
AC	Q23969		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Cocaine-sensitive serotonin transporter.		
GN	SEPT OR CG4545.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Corey J.L., Quick M.W., Davidson N., Lester H.A., Guastella J.;		
RL	Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; U02296; AADI0615.1; .		
DR	FLYBase; FBgn010414; SEPT.		
DR	InterPro; IPR000175; Na/nttran_sympot.		
DR	Pfam; PF00209; SNF; 1		
DR	PRINTS; PR00176; NANBUSMPORT.		
DR	PRODOM; PD000448; Na/nttran_sympot; 1.		
DR	PROSITE; PS00610; NA_NEUTROTAN_SYMP_1; 1.		
DR	PROSITE; PS00754; NA_NEUTROTAN_SYMP_2; 1.		
DR	PROSITE; PS0267; NA_NEUTROTAN_SYMP_3; 1.		
SQ	SEQUENCE 581 AA: 65177 MW: ID39D07069C7CD2F CRC64;		

Query Match 73.7%; Score 2314; DB 5; Length 581;  
Best local Similarity 78.7%; Pred. No. 2.1e-180;  
Matches 424; Conservative 48; Mismatches 63; Indels 4; Gaps 2;

QY	36	RORETWAKKAEPFLAVGFAVDLGNWRREPYICXONGGAFLLPYVMLFFGLPLFFLE	95
DB	31	RTRETWGKAEPFLAVIGFAVDLGNWRREPYICXONGGAFLLPYVCLFLFFGLPLFFYME	90
QY	96	LALGQYHRCGLTLWLRICPALKGVGVAICMIDYGMVYNTIIGAVYLLASLASINS	155

```

Db      91  LALGCFHRGCGSLIMKRICPALKGVAICLIDIMGYNTIIIGMAVYVL---FASFTS 147

Qy      156  VLEPWTSCDNEMNTPLCTPVTSPOQNPNSNSTPAKEFFERNVLQHKNSGLDMDGIRKSLA 2155
      148  KLEPWTSCDNPMWNTENCMQVTSNFETLSTPAKEFFERKVLSEYKGNGLDMDGVPKPTLA 2078

Db      216  LCVFGEFVLYVFSLMKGVSACKVYVWVATLAPYVLLTLRGVTLPEATGEGIRYTLPE 2757
      208  LCVFGEFVLYVFSLMKGVSACKVYVWVATLAPYVLLTLIRGVSLPEADGICIRYTLPE 2676

Qy      276  MHLKNSKWIDAASQIFFSGLCPGEGTLLALSNNKFNNNCYRDALITSSINCLTSELAG 3355
      268  MHLKNSKWIDAASQIFFSGLCPGEGTLLALSNNKFNNNCYRDALITSSINCLTSELAG 3276

Db      336  FVTFVSVLGVNAHQNKSIENGVLEBPGVLFYIYPPALITMGVSFMAIIFPLMITIGLD 3956
      328  FVTFVSVLGVNAHQKSIDKVLLEGGLVFYIYPPALITMGVSFWSIIFPLMITIGLD 3878

Qy      396  STEFGLEAVTALCDEYPRVLGRHREVEFAVLLLEIYICALPTTYGGVYVLDLINVYGP 4455
      388  STEFGLEAMTALCDEYPRVIGRRRLPVLLLATIFLICALPTMYGGVYVNVNLFNYGP 4427

Qy      456  GLAILEVVEPAEAGVCWYGVDRFESDEVKTLGHTPGFMWRTCMYSISPVFLVLFVFSV 5155
      448  GLAILEVVEPAEAGVFMYPGVDRFESDEVQMLGSRKGLFWIRCMYISPVFLTIFFSI 5078

Db      516  LAHEEMLGCGYIYPPMSISIVGVWMTGYISCPILYIIKKLL-IPGNCINIKITQIRE 573
      508  MGKEMKGEEYIYPPDMSIYGVNAVSSVLLAIPMTIYIIKFFPASKGCGRQLQSLQFPE 566


```

## RESULT 2

ID	OGMA5:	PRELIMINARY:	PRT:	631 AA.
AC	OGMA5:			
DT	01-MAR-2001 (TREMblrel. 15, Created)			
DT	01-MAR-2001 (TREMblrel. 16, Last sequence update)			
DT	01-JUN-2002 (TREMblrel. 21, Last annotation update)			
DE	Serotonin transporter.			
OS	Ovis aries (Sheep).			
OC	Mammalia: Metazoa: Chordata: Vertebrata: Euteleostomi:			
OC	Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:			
NCBI_TaxID=9940:	Ovis.			
NCBI_TaxID=9940:				

RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97259585; PubMed=9105686;  
 Pabury J.F., Tseng Y.T., McCormical B., Penado K., Stephan M.,  
 Rudnick G.;  
 "Placental biogenic amine transporters: cloning and expression".  
 PL Brain Res. Mol. Brain Res. 45:163-168(1997).

RA Tsenq Y.-T., McGonigal B.;  
 RL Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases  
 DR EMBL, AF246893; AAC01287.1; -  
 DR InterPro; IPR002437; 5HT\_transporter.  
 DR InterPro; IPR000175; Na/ntan\_symport.  
 DR Pfam; PF003491; 5HT\_transporter; 1.  
 DR Pfam; PF00209; SNF; 1.  
 DR PRINTS; PR00176; NANEUSMPORF.  
 DR ProDom; PD000448; Na/ntan\_symport; 1.  
 DR PROSITE; PS00610; NA\_NEUROTAN\_SYM\_1; 1.  
 DR PROSITE; PS00754; NA\_NEUROTAN\_SYM\_2; 1.  
 DR PROSITE; PS0267; NA\_NEUROTAN\_SYM\_3; 1.  
 DR PROSITE; 631 AA; 70521 MW; 3FCBA93B5B2CB3 CRC64;

```
Query Match      53.5%; Score 1681; DB 6; Length 631;  
Best Local Similarity 53.2%; Pred. No. 9.8e-129;  
Matches 309; Conservative 103; Mismatches 153; Indels 16; Gaps 7  
  
Oy      6 APPPTA---PPDDPATTTAAOKSRKVVVSLTPARORETWAKKAERLLAVGCAVDLGNW 62  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
```

```

Db 4) AVPNPGAGDOTHISIPAANT---ALVAEVRH-BRETHGKKVDFLLSVIGYAVDIGNW 103
OY 63 RPPYICYONGGAEFLIPYCVMLLEGGELPFLIELALGOYHRCGLTLMKRICPALKVCY 122
Db 104 RPPYICYONGGAEFLIPYIMAFEGIPLEFWEYPLGQYHNRGNCISWTIKCPIFGKIGC 163
OY 123 ALCIMIDYMKMYNNTIIGWAVYYLLASLASINSVLPMTSCDKNENFPLCPYVSPQNP- 181
Db 164 ALCIAEFYIASYNTNTAMALYYLL---SSFTQPLMTSCENSWNQCTNVPSEDNITW 220
OY 182 - -NSSPPEKEFERNYLEQHKNGLDMDPIKPSLAFVCFVFLVYFSLMKGVRSAGV 239
Db 221 MLHSTSAEEFYRHHVLOHRSKGLDGLGSLMOLVLCIMFIIYIFSTMKGVKTSKV 280
OY 240 VWTATAPYVLLILLARGVLLPGATEGIRIYYLPPEMHKONSKVWIDASQIFESLGP 299
Db 281 VWTAFIPYIILLILLVRGATLPGMARGVLFYLRKPNMKLLETGWVWDDAAQIFESLGP 340
OY 300 FGLLLLSSTNKNNNCCYDALITSSINCLTSFLAGFYIESVLGYMAHVONKSTEEVLE 359
Db 341 FGVLLAFASYNKHNHCYDALVTSAYVNCMTSPFSGVFIPLVLYGMAEMKREDVSEVAKD 400
OY 360 -GGGLAYIYVPELIATMTGSMVMAIIFMLTLTGLDSTFGCELVANTALCDEYPRVLR 418
Db 401 AGSGLLEFYIAEIANMMPASTFEALYFELMLITLGLDFTFGELRCVITAYVADDEPHYMAK 460
OY 419 HREYFAVALLLFYICALPPTTYGGVYVLDLNNVGPGLALYFVFAAGVCWGVGVR 478
Db 461 RREFFVLGVITTEFPFSLVTLTFGGAYVYKLLIEEPATGPVTLVALLIENAVAFMFQINQ 520
OY 479 FSEEDRTMIGTHPGWFMTQWTSYIESVPLLVEFVSVAHEEMLGGEYTPSWSTYGVW 538
Db 521 FCLIDVEMLEFSGFMWKICWVAISPLFLFIFICSFLMSPPQLRFLRYDPBWSIILGYC 580
OY 539 MGTGVYSCIPLYIYKLLTTPGNCINR-IKTIQREYVSI 578
Db 581 IGTSSEFCIPYIYVLYLVTPGLERAKIKGTTPKTPPE 621

```

### RESULT 3

ID	PRELIMINARY:	PRT:	617 AA.
AD	08R212:		
DC	08R212:		
DT	01-JUN-2002 (TREMBL)	21	(Created)
DT	01-JUN-2002 (TREMBL)	21	(Last sequence update)
DT	01-JUN-2002 (TREMBL)	21	(Last annotation update)
DE	Norepinephrine transporter.		
GN	SLC6A2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
CC	NCBI_TaxID=10090;		
RR	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPRAIN-C57BL/6; TISSUE=PLACENTA;		
RA	Loebbe S.Y., Bonisch H., Bruns M.;		
RT	"Molecular cloning and functional expression of the murine		
RL	norepinephrine transporter cDNA."		
DR	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: A143987; CAD28195.1; "		
SQ	SEQUENCE 617 AA: 69227 MW: 559164124688F759C CRC64:		

Query Match:	51.9%;	Score 1629.5;	DB 11;	Length 617;
Best Local Similarity	52.1%;	Pred. No. 1.5e-154;		
Matches 310; Conservative	104;	Mismatches 124;	Indels 27;	Gaps 9;

QY 1 MPSPDAPPAFTAP ---FDLPATTAQ---KSRSVVSL-----TPARORETWAKKAER 47

Db 6 MNQVQVPELGAGAPLEPQPLRPCKTADLLVYKERNGVQCILLASODSAQPEPTTWGKKIDF 65

QY 48 LLAVVGFAVDLGVWVWFRPYTCYQNGGAGFLIPYCYMLLEFGLPFFLELALGOVNRGCL 107

Db 66 LLSVVGFAVDLAWVWFRPYTCYKNGGAGFLIPYTFLELILAMPFLYVELMALGOVNRGGA 125

[illegible]

RESULT 4			
09V7R0			
ID	09V7R0	PRELIMINARY;	PRT; 576 AA.
AC	09V7R0;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, last annotation update)		
DE	CG6380 protein.		
CN	DAT OR CG6380.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
CN	NCBI_TaxId=7227;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BERKELEY;		
RX	MEDLINE=20196006; Pubmed=10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yancopoulos L., Zhang L.X.,		
RA	Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,		
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA	Abvill J.F., Abghyan A., An H.-J., Andrews-Plankkoch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,		
RA	Besson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,		
RA	Botkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,		
RA	Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Fowler K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,		
RA	Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris J.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Idegyam C.,		
RA	Jatall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kavalitz S., Kuip D., Lai Z.,		

RA Liao P, Lei Y, Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Lin X., Mattei B., McIntosh T.C., Meleod M.P., McInchessy D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshnefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,  
 RA Palazzolo M., Plattman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinett K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,  
 RA Styrbasas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Welnslock G.M., Weissensbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003806; AAF57966.1; -;  
 DR FlyBase: FBgn0034136; DAT.  
 DR InterPro: IPR000175; Na/nttran\_sympport.  
 DR Pfam: PF00209; SNF: 1.  
 DR PRINTS: PR00176; NANEUSMPORT.  
 DR Prodom: PD000448; Na/nttran\_sympport; 1.  
 DR PROSITE: PS00610; NA\_NEUTROTAN\_SYM\_1; 1.  
 DR PROSITE: PS50267; NA\_NEUTROTAN\_SYM\_3; 1.  
 Q0 SEQUENCE 576 AA; 64302 MW; 3606B72FEE57F909 CRC64;

Query Match	51.5%	Score 1618;	DB 5;	Length 576;
Best Local Similarity	54.5%	Pred. No. 1.2e-12;		
Matches 292; Conservative	96;	Mismatches 128;	Indels 20;	Gaps 4;

[illegible]

```

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Dopamine transporter.
CS DAT OR CG8380.
ON Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HEAD:
RA Porzgen P., Sonders M.S., Reed A.I., Ingram S.L., Amara S.G.;
RT "Identification of neurotransmitter transporters from Drosophila
  melanogaster.";
RL Abstr. - Soc. Neurosci. 25:160-160(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-HEAD:
RA Porzgen P., Park S.K., Hirsh J., Sonders M.S., Amara S.G.;
RT "An antidepressant-sensitive dopamine transporter from Drosophila
  melanogaster.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF260833; AAF76882.1; -.
DR FlyBase; FBgn0034136; DAT.
DR InterPro; IPR000175; Na/nttran_symport.
DR Pfam; PF00209; SNE; 1.
DR PRINTS; PR00176; NANEUSPORT.
DR PRODOM; PD000448; Na/nttran_symport; 1.
DR PROSITE; PS00610; NA_NEUTROTRAN_SYMPT_1; 1.
DR PROSITE; PS50267; NA_NEUTROTRAN_SYMPT_3; 1.
SQ SEQUENCE 631 AA; 70349 MW; AAF3B53F5A91ED89 CRC64;

```

Query Match	51.4%	Score 1615.5	DB 5	Length 631
Best Local Similarity	51.5%	Pred. No. 2.2e-123		
Matches	296	Conservative 99	Mismatches 137	Indels 43
			Gaps	5
QY	37	QRETWARKAEFLAVGVAVDGLGNVWREPRICYONGGGAFLIPYCVMLFGPLFLEL	96	
Db	26	ERETWSKGVDELTVSIVGPAVDLAWVWREPRICYKNGGAFLLVPYGMVGLVPLEYVEL	85	
QY	97	ALGGYHRCGLITLMKKRICPALKGVYACIMDITMGATNTITIGMAVYLLIASLASTNSV	156	
Db	86	ALGGHNRKGAITTCGRVLPEFGKIGYAVLLIAFYVDFFYNNIIAMSLEFFPASFET--NS-	142	
QY	157	LPMTSCNENMTPICTPYTSP-----	184	
Db	143	LPMTSCNINMTPICTPYTSP-----	184	
QY	185	-----TPAKEFERNVLEQHSKSGNDMDGPIKPSALCVGFVLFYFSFLMKGVRSAG	237	
Db	203	GHWGFGSASEYENRYILELRSEGIHDIGAIKMDMLCLLIYLLCYFSLMKGISNSG	262	
QY	238	KVVWVTALAPYVVLIIILLARGVTLPGATEGIRYTLTPEMHKLQNSKWMIDAQSITFSLG	297	
Db	263	KVVWVTALFPYAVLLIILLIRGLTLPGLSGLIQYLLTPNFSAIYKAAEWVADATQVFFSLG	322	
QY	298	PGFSTLLASISYKFNKNNCYRDALITISINCLTFSLAGVFYSVLGVMAHONKSIEPVG	357	
Db	323	PGFVLLAYASYNKHNHNYKDALTISFINATSFIAQVFYSVLGVMAHNLGYRIEDVA	382	
QY	358	LEGGGLVFYIYPEAIATMTGSFWAIIFFMLLITLIGDSTFGGLEAVYTTALCDEYPRVLG	417	
Db	383	TEGGGLVFYIYPAIATMTGASTFWALLFFMWLLTLLIGDSSRFGSEAITLIDSEPRK-K	441	
QY	418	RHRVEFPAVLLFIYICALPTTYGGYLVLDLWVYBGLAILEVYREAAAGVCWGYVD	477	
Db	442	RNRLEFPAAGLESLFVYVGLASCTGGGFEFFHLDRYAAGYSILAAVFEEAFAVSMYGTN	501	
QY	478	RFSEDVPTMLGHPGEMFRWCMSISPELPLVLVFSVSLAAHEMGVYTPMSISYNG	537	
Db	502	RFSIDIDMGHPGGRITWQCMREVALPFLLETFYVGLIGIEPLTADYVPSNANALGW	561	

```
Qy      538 VMGTGTVSCPLYYIIKKLLITPNCNICRITQRP 572
      : ::| || |::|| ||: |
Db      562 CIAGSSVVMIPAVAIFKLLSTPESLRQRFTLLTP 596
```

RESULT 6	
0961H9	PRELIMINARY; PRT; 631 AA.
ID 0961H9	
AC 0961H9	
DT 01-DEC-2001 (TREMblrel. 19, Created)	
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)	
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)	
DE GHZ2929P (Dopamine transporter).	
GN DAT OR CG8380.	
OS Drosophila melanogaster (Fruit fly).	
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC Ephydroidea; Drosophilidae; Drosophila.	
OX NCBI_TaxID=7227;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=BERKELEY;	
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,	
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,	
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,	
RA Nuno J., Paolel J., Paragas V., Park S., Phouanavong S., Wan K.,	
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;	
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	

RA SEQUENCE FROM N.A.  
 RA Gu H.H., Wu X.;  
 RT "Phenylalanine 105 in transmembrane domain 2 of the dopamine  
 transporter is involved in cocaine binding.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY051579; AAK93003.1; -  
 DR EMBL: AF439752; AAL32055.1; -  
 DR FLYBase: FBgn0034136; DAT.  
 DR InterPro: IPR000175; Na\_nlttran\_symport.  
 DR Pfam: PF00209; SNF; 1.  
 DR ProDom: PD000448; Na\_nlttran\_symport; 1.  
 DR PROSITE: PS00610; NA\_NEUOTRAN\_SYM\_1; UNKNOWN\_1.  
 DR PROSITE: PS50267; NA\_NEUOTRAN\_SYM\_3; 1.  
 SO SEQUENCE 631 AA; 70330 MW; E7583D17F81E31E6 CRC64;

Query Match	Similarity	Score	DB 5:	Length	631:
Best Local	51.5%	Pred. No.	2.2e-133		
Matches	296;	Conservative	99;	Mismatches	137;
				Indels	43;
				Gaps	5;

```

QY 37 QRETMAKKAETLLAVNGFAVDLGNWMPPTCYONGGAPLIPCVNLLTGGPLPFLLEL 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 ERETMWSKRVPLLSVIGFAVDLAVNMWPPYLCYNGGAPLVPYGLMVGIGLPIPYEML 85
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 ALGGYHRCGCTLLMKRICPALKGVAICMIDIMYGMWNTIIMAVYLLASLASINSV 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 86 ALGGHNKKGALITCGRLVPLEFGIGYAVLIAFYVDIYNYITMNSLRFFPAST--NS- 142
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 157 LPMTSCNENMTPLCTEPTSP-----OTNPNS----- 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 143 LPMTSCNNIMWTPNCRPFESQNASRVPYIGNYSDLYAMGNQSLLYNETYMNQSSLDTSAV 202
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 185 -----TPAKEFFERNVLEOHKNSGNDKMGPIKPSLALCVGYFVLVYTSLMKGVNSAG 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 GHVEGFOSASAEYFNRYLLELNRESEGHIDGALIMDPAALCLILLYLTSFSLMGISTSG 262
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 KVVWVNTLAPRVVLLILLAGCVTLPGATBEGIRYLTPEBHKLOMSKWIDAASOIFESLG 297
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 263 KVVWFETLFPYAVLLILLINGLTLPSSFLGIQYLLTNEFSAIKAEWVWDAATOVFESLG 322
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 PGFCTLLALSYSNFKNNCYRDALITSSINCTFLAGFYFVSVLGMAHONKSIEVGG 357
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 323 PGFQVLLATYASYNKYHNHYKDALITFSFINATSFIAGFYFVSVLGMAHTLGYRIEDVA 382
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 358 LGGGLVFIYVPEAIATMTGSVFMAIIFFLMLITLGLDSTFGGLEAVTALACDEYPRVLG 417

```





Query Match	51.1%	Score 1605	DB 6	Length 617
Best Local Similarity	51.6%	Pred. No. 1.5e-122		
Matches 299	Conservative 108	Mismatches 147	Indels 26	Gaps 8
OY	15	PDLPATNOKRSRVVS-----LTP-----ARQETWAKAEFLIAYVGAVDIGNTW	62	
DB	21	PEQPLRRARKTLELLVKKERNVQCLLPADGDQAPRETWGKKIDELLSVGFVAIDANW	80	
OY	63	RFPVICYONGGAFLIPYCVMLFEGLDFLELDELIGOVHRCGCTLMIRICPALKGAVY	122	
DB	81	RFPVICYONGGAFLIPYLPFLILINGMPLFEMELALGQNRGGAATVWK-ICPFEFGVGY	139	
OY	123	AICMIDIYGMATYNTIIGMAVYYLLASLASINSVLPWISCDNEWNTPLCT-----PVT	175	
DB	140	AVILALYGVGYNYNIAMSLYLTFSSP-TLN-LPWFECGHTWNSPNCIDPKLLNGSVL	196	
OY	176	SPQT--NNSSPRAKEFEERNVLEQHKSNGLDDMPKPSLACFGVGVLYVFSIMKGV	233	
DB	197	GNHTYSKRYKFTPAAEFEYERGLHHESSGHHIDIGIPQQLLCLMVAVVVLYTFSIMKGV	256	
OY	234	RSAGKVVWVWTLAPLVVLLILDLARGVTLPGATEGIRYVLTPEMKHLONSKWVDAASQIF	293	
DB	257	KTSGVNVVITATLPYFVLEVLLVHGVTLPGASNGINAYLIDIFYRLKATVWIDAATQTF	316	
OY	294	FSLGPGFTLLALSSYNKFNNNCYDALITSSINCLTSLFAGVFIYSVIGYMAHVONKSI	353	
DB	317	FSLGPGFVLLAFASYNKFNNDNNCYDALITSSINCLTSLFAGVFIYSVIGYMAHEKVIN	376	
OY	354	EEVLEGEGVFIYVPEAIATMTGVSFMAIIFFMALITIGLDSTGGLEAVNTALCDEP	413	
DB	377	EDVATEGAGVFIILPEAISTLGSSTFAVAVFIMILALGIDSSMGMEAITTGLADDF-	435	
OY	414	RVLGRFVFAVAVLLFTFYICALPTTGGGVVLDVLDLNYGGLAILFVPAAGVCWV	473	
DB	436	OYLKRHRKRLFTPGVYFTGFTLLAFCTTGIGIVYLLDFFAAGTSLTFVLMGAIGVSWF	495	
OY	474	YGVDRFSEDEVRTMLGHTPGEWERTQMSYISPVFLVLEFVSVAHEMLGEGEYTPSWSI	533	
DB	496	YGVDRFSNDIDQOMGFRGLYWRCLCMKFVSPALFLEVVVVSIINFRPLTYDDYIIPPMAN	555	
OY	534	TVGVWMTGTIVSCLPIIYIKLLITPGNCINIKITQIRE	573	
DB	556	VWGMGIALSMVLIPIYVIYIKFLSTQGSIMERLAVGITPE	595	
RESULT 11				
	063380			
	063380	PRELIMINARY:	PRT:	617 AA.
	063380:			
RC	01-NOV-1996	(TREMBlrel. 01, Created)		
DT	01-NOV-1998	(TREMBlrel. 08, Last sequence update)		
DT	01-JUN-2002	(TREMBlrel. 21, Last annotation update)		
DE	Norepinephrine transporter (NaCL-dependent norepinephrine transporter).			
DE	NET.			
GN	Rattus norvegicus (rat).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxId=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PHEOCHROMOCYTOMA;			
RA	Brussel M., Poerzgen P., Bryan-Lluka L.J., Boenisch H.,			
RL	Submitted (Nov-1997) to the EMBL/Genbank/DBD databases.			
RP	[2]			
RC	SEQUENCE OF 340-496 FROM N.A.			
RC	TISSUE=PHEOCHROMOCYTOMA;			
RC	MEDLINE=95341278; PubMed=7616203;			
RA	Cubellis J.F., Kim K.S., Baker H., Volpe B.T., Chung Y., Houpt T.A.,			
RA	Wessel T.C., Joh T.H.,			
RT	"Differential in vivo regulation of mRNA encoding the norepinephrine			
RT	transporter and tyrosine hydroxylase in rat adrenal medulla and locus			
RT	ceruleus";			

Query Match	50.9%	Score 1597.5	DB: 11	Length 617
Best Local Similarity	51.8%	Pred. No. 6,2e-122		
Matches	299	Conservative 105	Mismatches 150	Indels 23
			Gaps 8	
15	PDLPAATQ-----KSRVSVSLT-----PARQRETMARAEFLAVGVFAVDLGNVWFP	65		
Db	24	PLRPEKTDALLVYKRNNGVQCILASQDDAQDQRETMKGEIDFLSVGFADVLANVWFP	83	
QY	66	YICVONGGAGLIPYCVMLFEGDLFLELALGOYHRCCLTLMKRICPALKGVATC	125	
Db	84	YLCYKNGGAGLIPYTLFLILAGMPLFMELALGQFNREGATVWK-ICPEFGGVATV	142	
QY	126	MIDIWMGVYNTIIGMAVYVILASLASVNSVLPMTSCNENMTPLCT-----PVTSQ	178	
Db	143	LIALVGVYNTIAMSLLYLFASF-TLN--LPMTNCGAMNSPCTDPKLNASVLCDH	199	
QY	179	T--NPNSSTPAKKEPERENVLEQHKNGLDMDGPIKPSIALCVGFVLYVFSYKMGVRS	236	
Db	200	TKYSKXKTPAAEFYERGVHLHDESSGIDHIGLPMOLLCLMVYIVLVFSYKMGVRS	259	
QY	237	GKVWVWVATAPVVLILLARGVTLPGATEGIRYLTLPBWKLNQSKWIDAASQIFSL	296	
Db	260	GKVWVWVATAPVVLILLARGVTLPGASNGINATLHIDFYRLKATVATDAATDIFSL	319	
QY	297	GGGFTLLALSSYKFNENNCYDALITSSINCLTSFLAGVYFVSYGMAHVNQKSEEV	356	
Db	320	GAGFEVLLAFASYNKFNEDNCCYDALITSTINCVTSFISGFAFLSLTGMAHKKYIDV	379	
QY	357	GLEGFLVYVPEAIAITMGTSVEMAIIFPLMLITGLDSTFGLEAVTALCDEYPRVL	416	
Db	380	ATEGAGLVYVPEAISTLSGSTFMAVYLFMLLALIGDSSMGMEAVITGLADF-OVL	438	
QY	417	GRHREFAVALLFLFYCALPTTGGVYVLDLVWYPGALILVNVAAAGYGVWYV	476	
Db	439	KRHRKLFCAVILGFLFLAMFCITGGIYVILDLTPFAGSILPVALMEALGVSFWPYGV	498	
QY	477	DFRSEDEVTLGHTPGMFWRTGWSYISPEVFLVLFVSVLAHEMLAGEYTPYPSNITVG	536	
Db	499	DFRSDIOQMGMFGKGLWRLCMKRVSPAFLLFVWVSVIINEKPLTYDDYVYPPMANWVG	558	
QY	537	WVMGTGYSCIPLIYIKLLITPGNCIRIKRIOPE	573	
Db	559	WGIALSSMLVPAVYVYKFFSIRGSLMERVAVGITPE	595	

RESULT 12

Q9WTR3

PRELIMINARY: PRT: 567 AA.

Q9WTR3: 09WTR3: 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)

DR 01-JUN-2002 (TREMBlrel. 21, last annotation update)

DE Norepinephrine transporter a (rNeta).

OS Rattus norvegicus (rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxId=10116;

RP SEQUENCE FROM N.A.

RP MEDLINE=99214137; PubMed=101961444; 50.9% Score 1597.5; DB: 11; Length 617; Best Local Similarity 51.8%; Pred. No. 6,2e-122; Matches 299; Conservative 105; Mismatches 150; Indels 23; Gaps 8





RP [1]  
RC SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE-99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode *C. elegans*: a platform for  
RT investigating biology. The *C. elegans* Sequencing Consortium.";  
RT Science 282:2012-2018(1998).  
RP [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA "tin-wollam A., Becker M., Graves T.";  
RT "The sequence of *C. elegans* cosmid Y34E10B.";  
RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
RT "Direct Submission.";  
Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
EMBL: AC024812; AAF59549.2;  
InterPro: IPR00175; Na/ntran\_symport.  
Pfam: PF00209; SNF; 1. Nucleoside transport.  
DR PRINTS: PR00176; Nucleoside transport.  
DR PRODOM: PD000448; Na/ntran\_symport; 1.  
DR PROSITE: PS50267; Na-NEUROTRAN\_SYMPT\_3; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 671 AA: 75025 MW: 3A561F5559280C9E CRC64;

Query Match 50.5%; Score 1585.5; DB 5; Length 671;  
Best Local Similarity 48.9%; Pred. No. 6,5e-121;  
Matches 301; Conservative 110; Mismatches 160; Indels 45; Gaps 11;

QY 9 APTAPPDLPATTAOKSRSSVVS-----LTPARQ-----RE 39  
DB 43 APTA-SEYMPLSVAKPPLTVSTSHSIDPNEPIALGSLPTTKGKRAVALRRSSMW 101  
QY 40 TWAKKAEEFLAVGAVDGNVWRPPYICYONGGAFILPYCVMLFGPLFLELALG 99  
DB 102 KWATMEFLAVGAVDGNVWRPPYICYONGGAFILPYCVMLFGPLFLELALG 161  
QY 100 OYHRCGCLTLMKRICPALKGVGYAICMIDYMGWYNTIIGNAVYYLLASLAST-NSVLP 158  
DB 162 OFHRCGCVSIWKRKVCPLFRGIGYICICTFATFYNAIAOYFAIVLSKIMDEVP 221  
QY 159 WTSCNENMTPLCTP---VTSPTNPNSSTPAKEFEERNVLEQHSNGLDDMGPIKPSLA 215  
DB 222 WASCNPNMTPRCSDDLNTVTSRNGTPLTTPSEERYLYKVLVQKSTGDDLGKVTSM 281  
QY 216 LCPGVFVLVYSLMKGVRSACKVWVWALADYVLLILARGVTLPGATGIRYRLPE 275  
DB 282 VCLLAVFIWYFALMKGPQSSGKIYWTATAYIILSILLIRGLLPGAKNGLYYVTPD 341  
QY 276 WHKLONSKYVIDAASQIFPSLPGFGTLLALSSYNNKFNNDYDALITSSINCLTSF 335  
DB 342 FEKLADPAVWSAAATQIFPSLPGFGVLLALSSYNDFNNDYDALITSSINCLTSF 401  
QY 336 FVIFSVLGMAYHAKVOKSIEE-VGLEGPGLVFIYVEALATMTGVSFWALIFFLMTITGL 394  
DB 402 CVFSTGLGMSLLTNKPINEVGEHDASLFIYVQALATMTGVSFWALIFFLMTITGL 461  
QY 395 DSTFGLEAVTTALCDEYPRVLGRHREVFVAVLLFIYICALPTTYGGVYVLDLNYG 454  
DB 462 DSTFGIEAFITGFCDE-SRFLSKNRKMFVLYICIIYFLSPALSYGGQFVIFPLEDEG 520  
QY 455 PELAILFVFAAGACVWYGVDRPSSEVDRYMLGHTPGWFMTGCSYSISPVFLVLFVS 514  
DB 521 VLSLVLEFVTCMIAWCFYGVDRPSSEVDRYMLGHTPGWFMTGCSYSISPVFLVLFVS 579  
QY 515 VL--AHEEMLGEYTYPSWISIVGWMTGTVSCIPLYIYKLLITPGNCIRIKTIORP 572  
DB 580 VYNSSFKPIQMASYTFPMWSVILGWFLLRLSLVALIPVFAIYLLSGTGFLYERFWATTP 639

QY 573 E-----VTSIPPADST 583  
DB 640 QOQRNSATSL-AADPT 654

RESULT 15  
Q963F3 PRELIMINARY; PRT; 671 AA.  
AC Q963F3;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Serotonin reuptake transporter.  
GN MOD-5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ranganathan R., Sawin E.R., Trent C., Horvitz R.;  
RT "Mutations in the *C. elegans* Serotonin Reuptake Transporter MOD-5  
RT Reveal Serotonin-Dependent and -Independent Activities of  
RT Fluoxetine.";  
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF385631; AAK84832.1;  
DR InterPro: IPR00175; Na/ntran\_symport.  
DR Pfam: PF00209; SNF; 1.  
DR PRODOM: PD000448; Na/ntran\_symport; 1.  
DR PROSITE: PS50267; Na-NEUROTRAN\_SYMPT\_3; 1.  
SQ SEQUENCE 671 AA: 75037 MW: 8C1F180EBC9100A1 CRC64;

Query Match 50.3%; Score 1579.5; DB 5; Length 671;  
Best Local Similarity 48.7%; Pred. No. 2e-120;  
Matches 300; Conservative 110; Mismatches 161; Indels 45; Gaps 11;

QY 9 APTAPPDLPATTAOKSRSSVVS-----LTPARQ-----RE 39  
DB 43 APTA-SEYMPLSVAKPPLTVSTSHSIDPNEPIALGSLPTTKGKRAVALRRSSMW 101  
QY 40 TWAKKAEEFLAVGAVDGNVWRPPYICYONGGAFILPYCVMLFGPLFLELALG 99  
DB 102 KWATMEFLAVGAVDGNVWRPPYICYONGGAFILPYCVMLFGPLFLELALG 161  
QY 100 OYHRCGCLTLMKRICPALKGVGYAICMIDYMGWYNTIIGNAVYYLLASLAST-NSVLP 158  
DB 162 OFHRCGCVSIWKRKVCPLFRGIGYICICTFATFYNAIAOYFAIVLSKIMDEVP 221  
QY 159 WTSCNENMTPLCTP---VTSPTNPNSSTPAKEFEERNVLEQHSNGLDDMGPIKPSLA 215  
DB 222 WASCNPNMTPRCSDDLNTVTSRNGTPLTTPSEERYLYKVLVQKSTGDDLGKVTSM 281  
QY 216 LCPGVFVLVYSLMKGVRSACKVWVWALADYVLLILARGVTLPGATGIRYRLPE 275  
DB 282 VCLLAVFIWYFALMKGPQSSGKIYWTATAYIILSILLIRGLLPGAKNGLYYVTPD 341  
QY 276 WHKLONSKYVIDAASQIFPSLPGFGTLLALSSYNNKFNNDYDALITSSINCLTSF 335  
DB 342 FEKLADPAVWSAAATQIFPSLPGFGVLLALSSYNDFNNDYDALITSSINCLTSF 401  
QY 336 FVIFSVLGMAYHAKVOKSIEE-VGLEGPGLVFIYVEALATMTGVSFWALIFFLMTITGL 394  
DB 402 CVFSTGLGMSLLTNKPINEVGEHDASLFIYVQALATMTGVSFWALIFFLMTITGL 461  
QY 395 DSTFGLEAVTTALCDEYPRVLGRHREVFVAVLLFIYICALPTTYGGVYVLDLNYG 454  
DB 462 DSTFGIEAFITGFCDE-SRFLSKNRKMFVLYICIIYFLSPALSYGGQFVIFPLEDEG 520  
QY 455 PELAILFVFAAGACVWYGVDRPSSEVDRYMLGHTPGWFMTGCSYSISPVFLVLFVS 514  
DB 521 VLSLVLEFVTCMIAWCFYGVDRPSSEVDRYMLGHTPGWFMTGCSYSISPVFLVLFVS 579  
QY 515 VL--AHEEMLGEYTYPSWISIVGWMTGTVSCIPLYIYKLLITPGNCIRIKTIORP 572

Db	580	VYNSSEKPIOMASYTFPMWSYTLGWFRLSLAIPVPAITYLLSGTGTLYERFRWATP	639
Qy	573	E-----VTSIPPADST	583
Db	640	QQRNSATSL-AADPT	654

Search completed: July 18, 2003, 22:00:33  
Job time : 53 secs